

FIG. 1

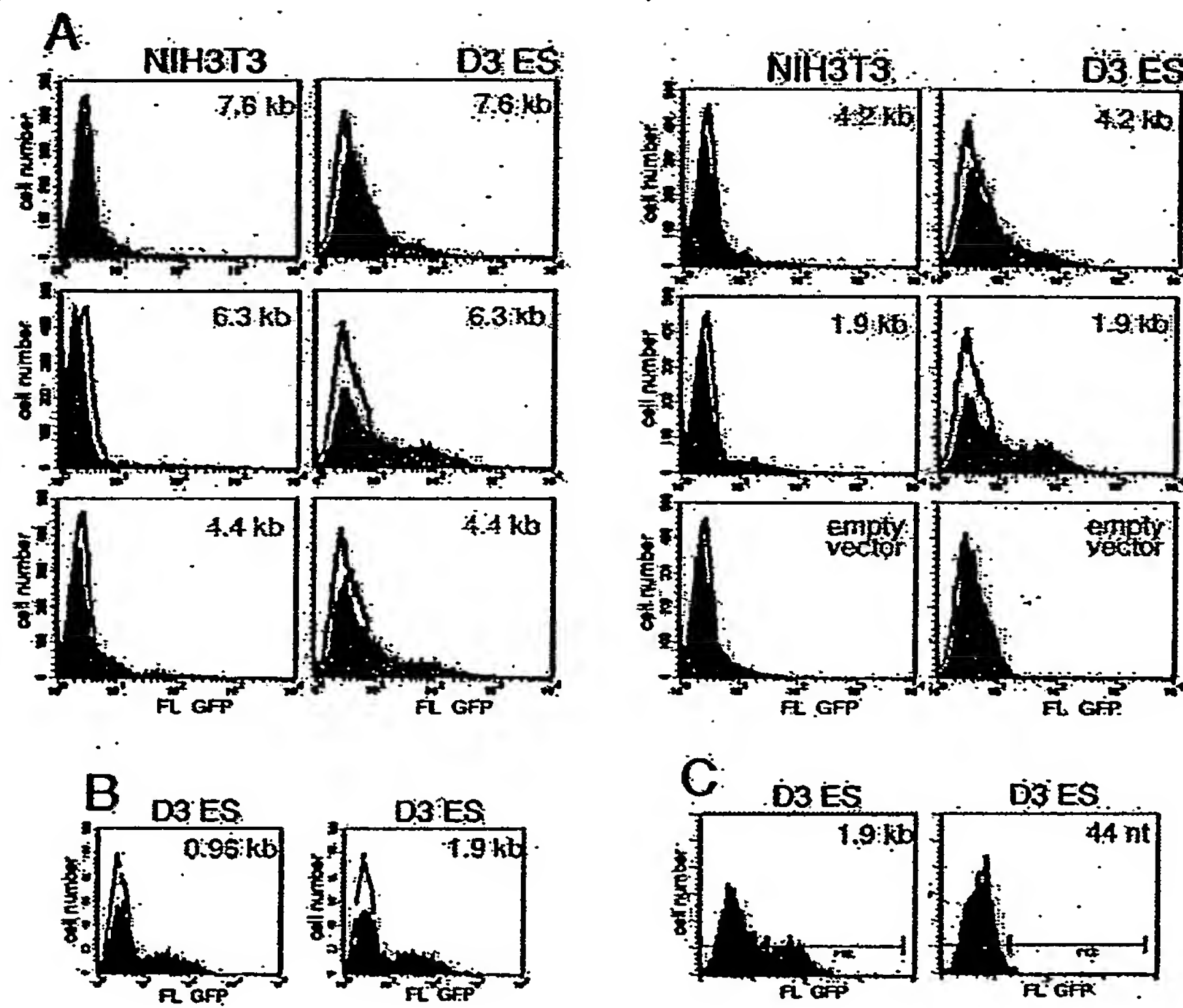


FIG. 2

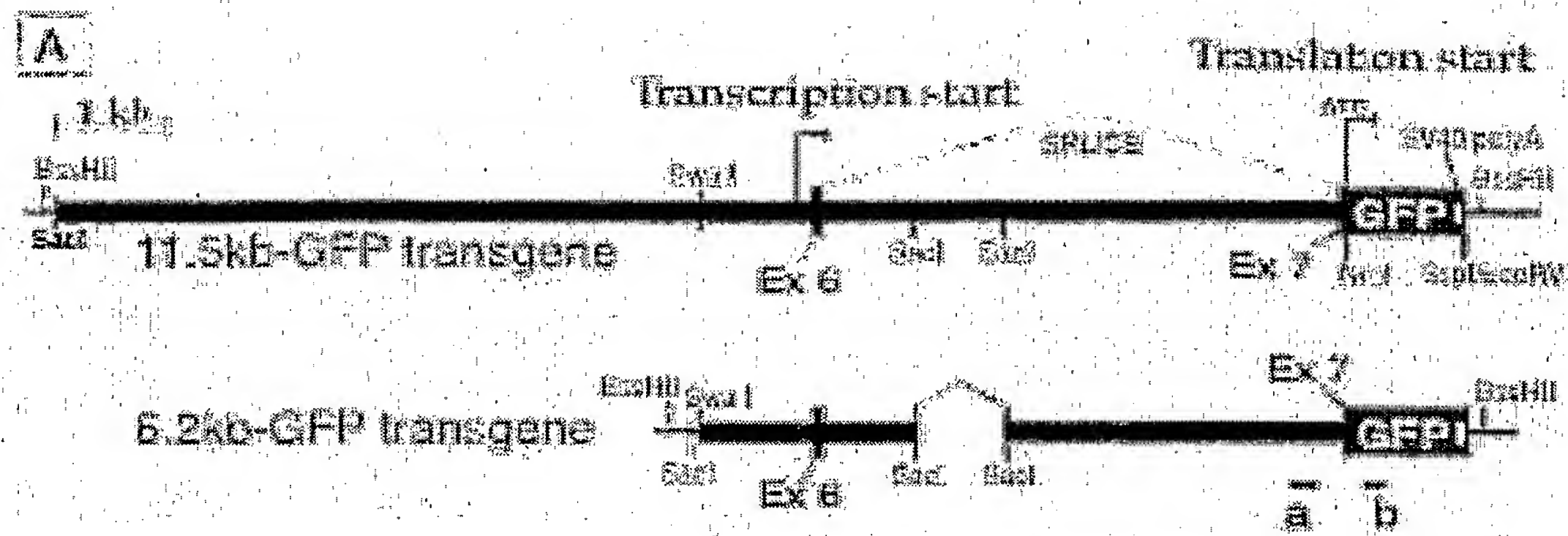


FIG. 3A

TRANSGENE COPY NUMBERS

transgene	Line	# copies
11.5 kb-GFP	A	5
"	C	13
"	D	11
6.2 kb-GFP	Z	17

FIG. 3B

-600 AGAAGTGATCTGGGCTGGACAGACTAGCTGAACTGGCCAGCTCTGGGTTCT
-550 ATCAAGAAACCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT
-500 AATGTCAACCTCAAAC Areb6 CCCTACCTGCATGTGCACACACATACATCCACA
-450 CACACACACACACACACACACACACACCACACACACACACACAA
-400 Nkx3.1 Fox factor binding sites ATAAATAAGTAAATAAATAAAATATTTAGCTCTCCAGACCAAATCTTGGT
-350 GAAACC Oct4 CATTTG Pax8 CATTTGTGTGTCTTACAAACACTGAAGGTTAA
-300 GAAGCATGCTCCTTAGTAATTTTATAGCAGTTTGCCTTTCCAGATTGAAA
-250 ACAGATTCTATAGGCTACACAGTGCTAAATGGATTATGCTCAGATACAGA Gata / Lmo2
-200 TTGAAAAGGATACAGATTGAAAAGGGTCGGGGTCTGGGC CAGGATGACGG Smad3/4
-150 GCCAACTATCTTTGCCCGGGCTTGTCCTT p53 Stat1/5 CAGGGAAGGGTTACAGGATTCT
-100 ACCACTGGGGTGTGGCCTATCTGCTGTTAGGACCTGAATTGCCTGGAGTG Gata / Lmo2
-50 Initiator TTTCTAGTTCCCACTAGTTGTTGAACTTTACCTTGAACCTCTGCTCCCAG stem-SHIP region

FIG. 4

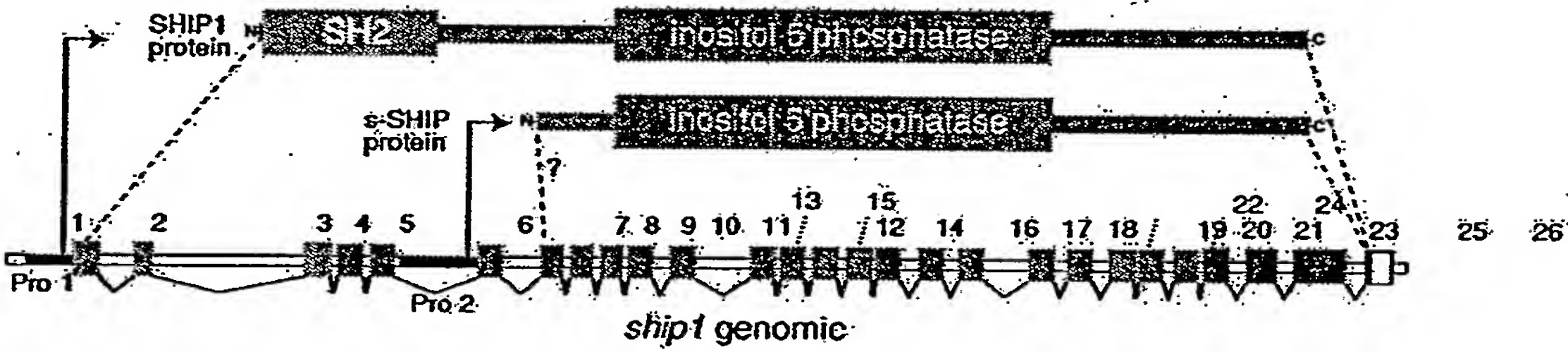


FIG. 5

CLUSTAL W (1.82) multiple sequence alignment

Hu	-----AGCCCGAGGATTGGAGTTGTCAATGGATGTGACAATGGGAAAATCCGTCT	50
Mo	CTCTGGGTTCATCAAGAAACCCTACCTCCATAACATAAAGTGTGATGGAGAAAGGCACCT	60
Hu	GAGCCTGCATTGTTGGGCTGCTAGGAGGGGATTGTCAT-CAGA-ATCCACAGATCACCAGCA	108
Mo	AATGTCAACCTCAAACCCCTACCTGCATGTGCACACACATACATCCACACCAACACACACA	120
Hu	C-TGGGCAGCCCTA---ATATTTAATAATGCAGATTCTAGACTCAATCAGGCGGGAGCCCA	164
Mo	CACACACACACAC CACACACCACACACACACACACACACAAATAAATAAGTAAATAAATAA	180
Hu	GAAATTTGCATTGTTAACACCTGTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	224
Mo	AATATTTA-GCTCTCCAGACCAAATCTTGGTGAAACCCATGCATTTCATTTCATTTCATTTC	239
Pax8		
Hu	TTTATAAACACAGAAGGTTGGGAACCATGGA---TAACTAAGTGAAGTCATTTTGTCACT	281
Mo	CCTACAAACACTGAAGGTTAAGAAGCATGCTCCTTAGTAATTTCATATAGCAGTTTGCCTTT	299
Hu	C-AGATTTGAATT---TTCTACAGGCTATAGAGTGCAGTTTGGCTAAAGCAAAACCTAGG	337
Mo	CCAGATTGAAAACAGATTCTATAGGCTACACAGTGCTAAATGGATTATGC-----TCAGA	354
Smad 3/4		
Hu	TACAGTCAGGACTACACAATTCAGTTTCGCTGTGGGTTGGGAAGGGATGGGTGGGCCCAGT	397
Mo	TACAGATTGAAAAGGATA----CAGATTGAAAAGGGTCGGG-----GTCCTGGGCCCAG-	402
P53 motif +/-		
Hu	GCTGGCAAGCCT-TGATCTTTGCCCGGGCTTGTCCTTCTGGGGAGAAATTACCTGCTTCTG	456
Mo	GATGACGGGCCAACTATCTTTGCCCGGGCTTGTCCTTCAGGGAAGGGTTACAGGATTCAC	462
STAT 1/5		
GATA/Lmo2		
Hu	CTGGACTGAGG-GTGCCCTCATCTCTGGCTAGAGCCCGTGCTGCCATGGAAGACTCTTTC	515
Mo	C---ACTGGGGTGTGGCCT-ATCTGCTGTTAGGACCTGAATTGCC-TGGAG---TGTTTC	514
Hu	CGGTGCCCACTAATCCTTGATGTTACCTTGT-CCCTGCCCCCAG	560
Mo	TAGTTCCCACTAGTTGTTGAACCTTACCTTGAACCTCTGCTCCCAG	560

FIG. 6

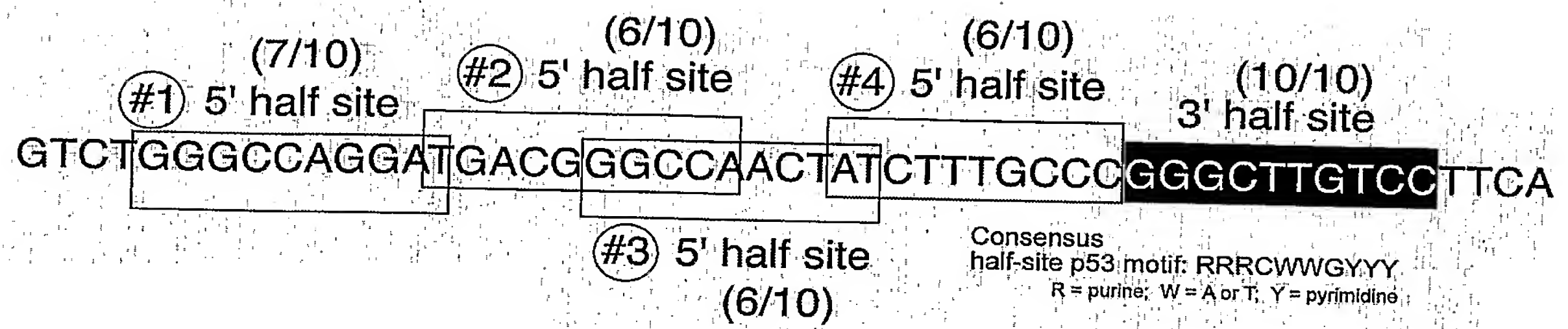


FIG. 7